Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (withdrawn): An isolated and purified compound having the structure of a human IgG binding pocket and comprising a first interacting surface, which is defined by the structure coordinates shown in Fig 1a for an IgG κ light chain for the amino acids Q124, S127, G128, T129, S131, V133, G157, N158, S159, Q160, E161, S162, S176, S177, T178, T180, and L181, and a second interacting surface, which is defined by the structure coordinates shown in Fig 1b for an IgG heavy chain for the amino acids P128, S129, L133, L150, K152, F175, P176, V178, L179, Q180, L184, L187 and S188, or a functional derivative of said compound.

Claim 2 (withdrawn): The compound of claim 1, wherein the second interacting surface is further defined by the structure coordinates shown in Fig 1 for an IgG heavy chain for the amino acids K126, F131, D153, S181, S182, and S186.

Claim 3 (withdrawn): The compound of claim 1, wherein the functional derivative of the compound has a root mean square deviation from the backbone atoms of the binding pocket amino acids of not more than 2.0Å.

Claims 4-5 (cancelled)

Claim 6 (withdrawn): An isolated and purified composite polypeptide consisting of one polypeptide consisting of a portion of a human IgG κ light chain starting at one of amino acids 93 to 110 and ending at one of amino acids 187 to 214 of human IgG κ light chain as set forth in SEQ ID NO:1 and one polypeptide consisting of a portion of a human IgG heavy chain starting at one of amino acids 106 to 128 and ending at one of amino acids 215 to 225 of human IgG light chain as set forth in SEQ ID NO:2.

Claim 7 (withdrawn): A polypeptide which comprises a binding pocket located between a first interacting surface, which is defined by the structure coordinates shown in Fig 1a for an IgG κ light chain for the amino acids Q124, S127, G128, T129, S131, V133, G157, N158, S159, Q160, E161, S162, S176, S177, T178, T180, and L181, and a second interacting surface, which is defined by the structure coordinates shown in Fig 1b for an IgG heavy chain for the amino acids P128, S129, L133, L150, K152, F175, P176, V178, L179, Q180, L184, L187 and S188.

Claim 8 (withdrawn): The polypeptide of claim 7, wherein the second interacting surface is further defined by the structure coordinates shown in Fig 1 for an IgG heavy chain for the amino acids K126, F131, D153, S181, S182, and S186.

Claim 9 (withdrawn): A complex comprising a ligand directly linked to the binding pocket of a polypeptide according to claims 6 or 7.

Claim 10 (withdrawn): The complex of claim 9, wherein the binding constant is at least 10^{-4} M.

Claim 11 (withdrawn): The complex of claim 9, wherein the molecule is a detectable label.

Claim 12 (currently amended): A method for evaluating the potential or ability of a chemical entity to associate with a human κ-Fab constant part-comprising composition, which method comprises providing a library of chemical entities and screening said library for ability to bind to the binding pocket of ~~a polypeptide according to claims 6 or 7~~ said human κ-Fab constant part-comprising composition; wherein said composition is a composite polypeptide consisting of one polypeptide consisting of a portion of a human IgG κ light chain starting at one of amino acids 93 to 110 and ending at one of amino acids 187 to 214 of human IgG κ light chain as set forth in SEQ ID NO:1 and one polypeptide consisting of a portion of a human IgG heavy chain starting at one of amino acids 106 to 128 and ending at one of amino acids 215 to 225 of human IgG light chain as set forth in SEQ ID NO:2.

Claim 13 (previously presented): The method of claim 12, further comprising testing a selection of the chemical entities that associate to said binding pocket by contacting them with a human κ-Fab constant part-comprising composition and grading said entities according to affinity.

Claims 14-25 (cancelled)

Claim 26 (new): A method for evaluating the potential or ability of a chemical entity to associate with a human κ-Fab constant part-comprising composition, which method comprises providing a library of chemical entities and screening said library for ability to bind to the binding pocket of said human κ-Fab constant part-comprising composition; wherein said composition is a polypeptide which comprises said binding pocket located between a first interacting surface, which is defined by the structure coordinates shown in Fig 1a for an IgG κ light chain for the amino acids Q124, S127, G128, T129, S131, V133, G157, N158, S159, Q160, E161, S162, S176, S177, T178, T180, and L181, and a second interacting surface, which is defined by the structure coordinates shown in Fig 1b for an IgG heavy chain for the amino acids P128, S129, L133, L150, K152, F175, P176, V178, L179, Q180, L184, L187 and S188.

Claim 27 (new): The method of claim 26, wherein said second interacting surface is further defined by the structure coordinates shown in Fig 1 for an IgG heavy chain for the amino acids K126, F131, D153, S181, S182, and S186.

Claim 28 (new): The method of claim 26, further comprising testing a selection of the chemical entities that associate to said binding pocket by contacting them with a human κ-Fab constant part-comprising composition and grading said entities according to affinity.